Proceedings of the SIGA Young Web Meeting
7 July, 2020
ISBN **978-88-944843-0-4**

Oral Communication Abstract – SY16

COMPARATIVE PROFILING OF AXILLARY BUDS FROM 'ON' AND 'OFF' BRANCHES REVEALS A COMPLEX GENE NETWORK IN *OLEA EUROPAEA*

FORGIONE I.*, SALIMONTI A.*, SIRANGELO T.M.*, PUCCIO G.**, MERCATI F.***, SUNSERI F.****, CARBONE F.*

*) Centro di ricerca Olivicoltura, Frutticoltura e Agrumicoltura, CREA, C.da Li Rocchi Vermicelli, 87036 Rende (Italy) - ivanoforgione@gmail.com
**) Dipartimento di Scienze Agrarie, Alimentari e Forestali, Università degli Studi di Palermo, Viale delle Scienze, 90128 Palermo (Italy)
***) Istituto di Bioscienze e BioRisorse (IBBR), Consiglio Nazionale delle Ricerche (CNR), Corso Calatafimi, 90129 Palermo (Italy)
****) Dipartimento di Agraria, Università Mediterranea di Reggio Calabria, Reggio Calabria (Italy)

The olive tree (*Olea europaea* L. subsp. *europaea* var. *europaea*) is a crop with a tendency of alternate bearing for fruit productivity, showing a high fruit load in a year ('ON year') followed by one characterized by limited or no yield ('OFF year'). This trait should be determined by complex pathways included into the journey from axillary buds to fruit, through flower development, driven by different endogenous and environmental stimuli. Molecular mechanisms involved in this process and relative networking until now remain unknown in olive. In this study, different RNA-seq libraries were generated from axillary buds of olive tree (cv. Leccino) branches classified as 'ON' and 'OFF' collected in July 2018 and March 2019. NGS sequencing generated about 370 M high-quality reads corresponding to 79,910 Unigenes. A total of 944 differentially expressed genes (DEGs) between 'ON' and 'OFF' branches were identified, with 317 significantly induced in the 'ON' branches and 627 in the 'OFF' branches, respectively. Among the upregulated genes in the 'ON' branches, 18% were detected in July, 79% in March and 3% were shared by both treatments; a similar trend was observed in the 'OFF' branches albeit with a marked reduction in the percentage of genes detected during sampling times: 47% in July, 50% in March and 3% shared between treatments. Our findings highlighted for the first time a different transcriptome profile between 'ON' and 'OFF' branches in olive, involving a wide group of genes associated to the flowering process. In particular, the differences displayed in March 'OFF' branches may address the axillary buds towards flower differentiation. Additionally, a wide set of DE genes related to hormonal, sugar and phenylpropanoid pathways was identified in buds collected in July and March. These genes could directly and indirectly modulate different pathways, suggesting their key role during the axillary bud differentiation.

Work supported by the Italian Ministry of agricultural food and forestry policies Project OLGENOME DM 13939 – 24/04/2018